



SEQUENCE LISTING

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<120> UMLR POLYPEPTIDES

<130> 99-75

<140> 09/695,369

<141> 2000-10-23

<150> 60/160, 880

<151> 1999-10-22

<150> 60/163, 215

<151> 1999-11-02

<150> 60/218,769

<151> 2000-07-17

<150> 60/222,221

<151> 2000-08-01

<160> 50

<170> FastSEQ for Windows Version 3.0

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<211> 1162

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (104)...(913)

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Met Asp Cys Gln	
1	
 gaa aat gag tac tgg gac caa tgg gga cgg tgt gtc acc tgc caa cgg	163
Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val Thr Cys Gln Arg	
5 10 15 20	
 tgt ggt cct gga cag gag cta tcc aag gat tgt ggt tat gga gag ggt	211
Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly Tyr Gly Glu Gly	
25 30 35	
 gga gat gcc tac tgc aca gcc tgc cct cct cgc agg tac aaa agc agc	259
Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg Tyr Lys Ser Ser	
40 45 50	
 tgg ggc cac cac aaa tgt cag agt tgc atc acc tgt gct gtc atc aat	307
Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys Ala Val Ile Asn	
55 60 65	
 cgt gtt cag aag gtc aac tgc aca gct acc tct aat gct gtc tgt ggg	355
Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn Ala Val Cys Gly	
70 75 80	
 gac tgt ttg ccc agg ttc tac cga aag aca cgc att gga ggc ctg cag	403
Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile Gly Gly Leu Gln	
85 90 95 100	
 gac caa gag tgc atc ccg tgc acg aag cag acc ccc acc tct gag gtt	451
Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro Thr Ser Glu Val	
105 110 115	
 caa tgt gcc ttc cag ttg agc tta gtg gag gca gat gca ccc aca gtg	499
Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala Pro Thr Val	
120 125 130	
 ccc cct cag gag gcc aca ctt gtt gca ctg gtg agc agc ctg cta gtg	547
Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser Leu Leu Val	
135 140 145	

gtg ttt acc ctg gcc ttc ctg ggg ctc ttc ttc ctc tac tgc aag cag 595
 Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr Cys Lys Gln
 150 155 160

ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct 643
 Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
 165 170 175 180

gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag 691
 Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
 185 190 195

gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc 739
 Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
 200 205 210

tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag 787
 Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
 215 220 225

ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag 835
 Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
 230 235 240

acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc 883
 Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
 245 250 255 260

aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaagag gtctcttggg 933
 Asn Val Pro Phe Glu Val Pro Ser Pro *
 265

cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc 993
 aggggcctga aatgtgatgt ccacaagagc taatacccta cagatggggc atatacctatc 1053
 ccatcccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct 1113
 tccctgttgt agtctgggga gccagattcc acatgcatgg ggcggccgc 1162

<210> 2

<211> 269

<212> PRT

<213> Homo sapiens

<400> 2

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Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly	20	25	30	
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg	35	40	45	
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys	50	55	60	
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn	65	70	75	80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile	85	90	95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro	100	105	110	
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp	115	120	125	
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser	130	135	140	
Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu	145	150	155	160
Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Gly	Gly	Leu	Leu	165	170	175	
Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro	Val	180	185	190	
Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Glu	Ser	Phe	Thr	Met	195	200	205	
Ala	Ser	Cys	Thr	Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	210	215	220	
Glu	Cys	Thr	Glu	Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	225	230	235	240
Thr	Gly	Ala	Glu	Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	245	250	255	
Arg	Leu	Glu	Leu	Asn	Val	Pro	Phe	Glu	Val	Pro	Ser	Pro				260	265		

<210> 3

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate sequence

<221> misc_feature

<222> (1)...(807)

<223> n = A,T,C or G

<400> 3

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tgyacngcnt	gyccnccnm	nmgtayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgtty	taymgnaara	cnmgnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtnccnc	cncargargc	nacnytnngtn	420
gcnytnngtnw	snwsnytnyt	ngtngtntty	acnytnngnt	tyytnnggny	nttyttyytn	480
taytgyaarc	arttyttyaa	ymgncaytg	carmgngngg	gnytnytnc	rttygargcn	540
gayaaracng	cnaargarga	rwsnytnntty	ccngtnccnc	cnwsnaarga	racnwsngcn	600
garwsncarg	arwsnttyac	natggcnwsn	tgyacnwsng	arwsncayws	ncaytgggtn	660
caywsnccna	thgartgyac	ngarytnngay	ytncaraart	tywsnwsnws	ngcnwsntay	720
acngngngcng	aracnytnng	nggnaayacn	gtngarwsna	cngngaymg	nytngarytn	780
aaygtncnt	tygargtncc	nwsnccn				807

<210> 4

<211> 41

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<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #1

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (19)...(20)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (22)...(26)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (27)...(30)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (32)...(37)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (38)...(39)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (41)...(41)

<223> Xaa is any amino acid residue

<400> 4

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Cys	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	
			20				25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa							
			35				40								

<210> 5

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #2

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(15)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (16)...(17)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (19)...(20)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (22)...(23)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (24)...(24)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (26)...(33)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (34)...(36)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (38)...(44)

<223> Each Xaa is independently any amino acid residue

<400> 5

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30	

Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 35 40 45

<210> 6

<211> 49

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #3

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(7)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (8)...(8)

<223> Xaa is any amino acid residue or not present

<221> VARIANT

<222> (9)...(14)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (15)...(18)

<223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT

<222> (20)...(21)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (23)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (25)...(29)

<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT

<222> (31)...(38)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (39)...(39)

<223> Xaa is any amino acid residue or not present

<221> VARIANT

<222> (41)...(47)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (49)...(49)

<223> Xaa is any amino acid residue or not present

<400> 6

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5					10						15		
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
			35				40						45			
Xaa																

<210> 7

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #3 alternative motif

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<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(7)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is independently any amino acid residue or not
present

<221> VARIANT
<222> (10)...(13)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (14)...(18)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (31)...(40)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (41)...(46)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (48)...(48)
<223> Xaa is any amino acid residue

<400> 7

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	
			35					40					45			

<210> 8

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #4

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (18)...(19)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (21)...(22)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (24)...(27)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (28)...(33)

<223> Each Xaa is independently any amino acid residue

or not present

<221> VARIANT

<222> (35)...(37)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (38)...(41)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (43)...(43)

<223> Each Xaa is independently any amino acid residue

<400> 8

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5					10						15		
Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa						
			35					40								

<210> 9

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #4 alternative motif

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
 <222> (18)...(22)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (24)...(27)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (28)...(33)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (34)...(37)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (38)...(41)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (43)...(43)
 <223> Xaa is any amino acid residue

<400> 9
 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40

<210> 10
 <211> 18
 <212> DNA
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<220>
 <223> oligonucleotide primer ZC25352

<400> 10
ccttgcccag ttgttctc 18

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25353

<400> 11
tctggtggga tgggatag 18

<210> 12
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25364

<400> 12
acctgtgctg tcatcaatcg tgttca 26

<210> 13
<211> 24
<212> DNA
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<220>
<223> oligonucleotide primer ZC25365

<400> 13
cccccaaggc ctcagctcca gtat 24

<210> 14
<211> 18
<212> DNA
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<220>
<223> oligonucleotide primer ZC25352

<400> 14
ccttgcccag ttgttctc 18

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC25353

<400> 15
tctggtggga tgggatag 18

<210> 16
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Artificial Protein

<400> 16
Glu Tyr Met Pro Met Glu
1 5

<210> 17
<211> 33
<212> DNA
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<220>
<223> oligonucleotide primer ZC25598

<400> 17
gcggatccga ttgccaagaa aatgagtact ggg 33

<210> 18
<211> 37
<212> DNA
<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC25596

<400> 18

gcagatctgg gctccactgt gggatcatct gcctcca

37

<210> 19

<211> 108

<212> DNA

<213> Homo sapiens

<220>

<223> tPA leader

<400> 19

atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggcgc cgtcttcggt
tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagatcc

60

108

<210> 20

<211> 693

<212> DNA

<213> Artificial Sequence

<220>

<223> Fc4 tag

<400> 20

agatcttcag	acaaaactca	cacatgccc	ccgtgcccag	cacctgaagc	cgagggggca	60
ccgtcagctt	tcctcttccc	cccaaaaccc	aaggacaccc	tcattgatctc	ccggaccctt	120
gaggtcacat	gcgtggtggt	ggacgtgagc	cacgaagacc	ctgaggtcaa	gttcaactgg	180
tacgtggacg	gcgtggaggt	gcataatgcc	aagacaaagc	cgcgggagga	gcagtacaac	240
agcacgtacc	gtgtggtcag	cgtcctcacc	gtcctgcacc	aggactggct	gaatggcaag	300
gagtacaagt	gcaaggctctc	caacaaagcc	ctcccatcct	ccatcgagaa	aaccatctcc	360
aaagccaaag	ggcagccccg	agaaccacag	gtgtacaccc	tgcccccatc	ccgggatgag	420
ctgaccaaga	accaggtcag	cctgacctgc	ctggtcaaag	gcttctatcc	cagcgacatc	480
gccgtggagt	gggagagcaa	tgggcagccg	gagaacaact	acaagaccac	gcctcccgtg	540
ctggactccg	acggctcctt	cttcctctac	agcaagctca	ccgtggacaa	gagcaggtgg	600
cagcagggga	acgtcttctc	atgctccgtg	atgcatgagg	ctctgcacaa	ccactacacg	660
cagaagagcc	tctccctgtc	tccgggtaaa	taa			693

<210> 21

<211> 534

<212> DNA

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<220>

<223> Polynucleotide Construct

<400> 21

atggatgcaa	tgaagagagg	gctctgctgt	gtgctgctgc	tgtgtggcgc	cgtcttcggt	60
tcgctcagcc	aggaaatcca	tgccgagttg	agacgcttcc	gtagatccga	ttgccaagaa	120
aatgagtact	gggaccaatg	gggacggtgt	gtcacctgcc	aacggtgtgg	tcctggacag	180
gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
gtcatcaatc	gtgttcagaa	ggtcaactgc	acagctacct	ctaattgctgt	ctgtggggac	360
tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttccagtt	gagcttagtg	480
gaggcagatg	caccacacagt	ggagcccaga	tctgaatata	tgcccatgga	ataa	534

<210> 22

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> construct

<400> 22

atggatgcaa	tgaagagagg	gctctgctgt	gtgctgctgc	tgtgtggcgc	cgtcttcggt	60
tcgctcagcc	aggaaatcca	tgccgagttg	agacgcttcc	gtagatccga	ttgccaagaa	120
aatgagtact	gggaccaatg	gggacggtgt	gtcacctgcc	aacggtgtgg	tcctggacag	180
gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
gtcatcaatc	gtgttcagaa	ggtcaactgc	acagctacct	ctaattgctgt	ctgtggggac	360
tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttccagtt	gagcttagtg	480
gaggcagatg	caccacacagt	ggagcccaga	tcttcagaca	aaactcacac	atgccaccg	540
tgcccagcac	ctgaagccga	gggggcaccg	tcagtcttcc	tcttcccccc	aaaaccaag	600
gacaccctca	tgatctcccc	gaccctgag	gtcacatgcg	tgggtggtgga	cgtgagccac	660
gaagaccctg	aggtaagtt	caactggtac	gtggacggcg	tggagggtgca	taatgccaag	720
acaaagccgc	gggaggagca	gtacaacagc	acgtaccgtg	tggtcagcgt	cctcaccgtc	780
ctgcaccagg	actggctgaa	tggcaaggag	tacaagtgca	aggctctcaa	caaagccctc	840
ccatcctcca	tcgagaaaac	catctccaaa	gccaaagggc	agccccgaga	accacagggtg	900
tacaccctgc	ccccatcccc	ggatgagctg	accaagaacc	aggtcagcct	gacctgcctg	960
gtcaaaggct	tctatcccag	cgacatcgcc	gtggagtggg	agagcaatgg	gcagccggag	1020

aacaactaca agaccacgcc tcccggtgctg gactccgacg gctccttctt cctctacagc 1080
 aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1140
 catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaataa 1200

<210> 23
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC26463

<400> 23
 atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct 47

<210> 24
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC26464

<400> 24
 taatacgact cactataggg aggggccctt gctgctgttg tggtat 46

<210> 25
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC26470

<400> 25
 atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca 49

<210> 26
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<223> Oligonucleotide ZC26471

taatacgact cactataggg agcccccaa ggtctcagct ccagtat

47

<211> 297

<213> Homo sapiens

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val
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Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
			20					25					30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
		35					40					45			
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
	50					55				60					
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65					70				75						80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
				85				90						95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
			100					105					110		
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp
		115					120					125			
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser
						135					140				
Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu
145					150					155					160
Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Gly	Gly	Leu	Leu
				165					170					175	
Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro	Val
			180					185					190		
Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu	Asn	Ile
		195					200					205			
Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser
		210				215					220				

Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr
225					230					235					240
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu
				245					250					255	
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu
			260					265					270		
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu	Glu	Leu
		275					280					285			
Asn	Val	Pro	Phe	Glu	Val	Pro	Ser	Pro							
	290					295									

<210> 28
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate sequence

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<221> misc_feature
<222> (1)...(891)
<223> n = A,T,C or G
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<400> 28

atggaytgyc	argaraayga	rtaytgggay	cartggggnm	gntgygtnac	ntgycarmgn	60
tgyggncng	gncargaryt	nwsnaargay	tgyggntayg	gngargggng	ngaygcntay	120
tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgntty	taymgnaara	cnmgcnathgg	nggnytncar	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtnargc	ngaygcncn	acngtnccnc	cncargargc	nacnytngtn	420
gcnytngtnw	snwsnytnyt	ngtngnttty	acnytngcnt	tyytnggnyt	nttyttyytn	480
taytgyaarc	arttyttyaa	ymgncaytg	carmgnggng	gnytnytnc	rttygargcn	540
gayaaracng	cnaargarga	rwsnynttty	ccngtnccnc	cnwsnaarga	racnwsngcn	600
garwsncarg	tnwsngaraa	yathttycar	acncarceny	tnaayccnat	hytnargay	660
gaytgywsnw	snacnwsng	nttyccnacb	cargarwsnt	tyacnatggc	nwsntgyacn	720
wsngarwsnc	aywsncaytg	ggtncaywsn	ccnathgart	gyacngaryt	ngayytnca	780
aarttywsnw	snwsngcnws	ntayacnggn	gcngaracny	tngngngnaa	yacngtngar	840
wsnacngng	aymgnytnga	rytnaayqtn	ccnttygarg	tnccnwsncc	n	891

<210>	29
<211>	267
<212>	PRT

<400> 29

<210> 30

<211> 801

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate sequence

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 30

atggaytgyc	argaraayga	rtaytgggag	cartgggggm	gntgygtnac	ntgycarmgn	60
tgyggncng	gncargaryt	nwsnaargay	tgyggntayg	gngarggngg	ngaygcntay	120
tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgntty	taymgnaara	cnmgcnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtnccnc	cncargargc	nacnytnngtn	420
gcnytnggng	gnytnytnca	rttygargcn	gayaaracng	cnaargarga	rwsnytnntty	480
ccngtnccnc	cnwsnaarga	racnwsngcn	garwsncarg	tnwsngaraa	yathttycar	540
acncarceny	tnaayccnat	hytnngargay	gaytgywsnw	snacnwsngg	nttyccnacn	600
cargarwsnt	tyacnatggc	nwsntgyacn	wsngarwsnc	aywsncaytg	ggtncaysn	660
ccnathgart	gyacngaryt	ngayytncar	aarttywsnw	snwsngcnws	ntayacnggn	720
gcngaracny	tnggnggnaa	yacngtngar	wsnacnggng	aymgnytna	rytnaaygtn	780
ccnttygarg	tnccnwsncc	n				801

<210> 31

<211> 529

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(529)

<223> n = A,T,C or G

<400> 31

ggattcnatn	nctgaggntg	natggcnttc	nagttnwgas	tkagtggagg	cagatgcasc	60
cacagtcccc	gcctcaggag	gycacacttg	ttgcrmtggt	gagcagcstg	ctagtgggtg	120
ttccctggc	cttctgggg	ctcttcttcc	tcwacycaa	gcagttcttc	aacagacatt	180
gycagcsng	gaggtttgct	gcagtttgag	gctgatraaa	cagcaaagga	ggaatctstm	240
ttycycgtgc	caccagcaa	ggagaccagt	gctgagtccc	aagtgagtga	gaacatyttt	300
cakaccagm	cacttaaccc	tatcctyrag	gacgactgca	rctcgactag	tgyttcccc	360
acacaggart	mctttaccat	ggcctyctgc	acctyagaga	gccactacca	ctgggwccac	420
arcccatcg	aatgcacaka	gctggacctg	caaaagtttt	ccagctctgc	ctctataact	480
ggagctgara	ccttgggggg	aaacacagnc	aaaagcactg	ganacaggg		529

<210> 32
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 32
 cagttgagct tagtgaggc agatgcaccc acagtgcccc ctcaggaggc cacacttggt 60
 gsactggagg tttgctgcag tttgaggctg ataaaacagc aaaggaggaa tctctcttns 120
 ccgtgccacc cagcaaggag accagtgctg agtcccaagt gagtgagaac atctttcaga 180
 cccagccact taaccctatc ctcgaggacg actgcagctc gactagtggc ttccccacac 240
 aggagtcctt taccatggcc tcctgcacct cagagagcca ctcccactgg gtccacagcc 300
 ccacgaatg cacagagctg gacctgcaaa agttttccag ctctgcctcc tatactggag 360
 ctgagacctt ggggggaaac acagtcgaaa gcactggaga c 401

<210> 33
 <211> 528
 <212> DNA
 <213> Homo sapiens

<400> 33
 ctctgagggt caatgtgcct tccagttgag cttagtggag gcagatgcac ccacagtgcc 60
 ccctcaggag gccacacttg ttgcaactgt gagcagcctg ctagtggtgt ttaccctggc 120
 cttcctgggg ctcttcttcc tctactgcaa gcagttcttc aacagacatt gccagcgtgt 180
 tgcaggaggt ttgctgcagt ttgaggctga taaaacagca aaggaggaat ctctcttccc 240
 cgtgccaccc agcaaggaga ccagtgtga gtcccaagtg agtgagaaca tctttcagac 300
 ccagccactt aaccctatcc tcgaggacga ctgcagctcg actagtggct tccccacaca 360
 ggagtccttt accatggcct cctgcacctc agagagccac tcccactggg tccacagccc 420
 catcgaatgc acagagctgg acctgcaaaa gttttccagc tctgcctcct atactggagc 480
 tgagaccttg ggggggaaaca cagtcgaaag cactggagac aggctgga 528

<210> 34
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 34

Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp Ala
 1 5 10 15
 Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser Ser
 20 25 30
 Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr
 35 40 45
 Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly Leu
 50 55 60
 Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro
 65 70 75 80
 Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn
 85 90 95
 Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys Ser
 100 105 110
 Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser Cys
 115 120 125
 Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr
 130 135 140
 Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala
 145 150 155 160
 Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 165 170 175

<210> 35

<211> 299

<212> PRT

<213> Homo sapiens

<400> 35

Met Asp Cys Gln Glu Asn Glu Tyr Trp Asp Gln Trp Gly Arg Cys Val
 1 5 10 15
 Thr Cys Gln Arg Cys Gly Pro Gly Gln Glu Leu Ser Lys Asp Cys Gly
 20 25 30
 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45
 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60
 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80
 Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
 85 90 95
 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
 100 105 110

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
 130 135 140
 Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
 145 150 155 160
 Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Val Ala Gly Gly
 165 170 175
 Leu Leu Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe
 180 185 190
 Pro Val Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu
 195 200 205
 Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
 210 215 220
 Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
 225 230 235 240
 Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
 245 250 255
 Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
 260 265 270
 Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 275 280 285
 Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 290 295

<210> 36

<211> 431

<212> DNA

<213> Homo sapiens

<400> 36

ctc tga ggt tca atg tgc ctt cca gtt gag ctt agt gga ggc aga tgc	48
acc cac agt gcc ccc tca gga ggc cac act tgt tgc act gga ggt ttg	96
ctg cag ttt gag gct gat aaa aca gca aag gag gaa tct ctc ttc ccc	144
gtg cca ccc agc aag gag acc agt gct gag tcc caa gtg agt gag aac	192
atc ttt cag acc cag cca ctt aac cct atc ctc gag gac gac tgc agc	240
tcg act agt ggc ttc ccc aca cag gag tcc ttt acc atg gcc tcc tgc	288
acc tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca	336
gag ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct	384
gag acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg ga	431

<210> 37

<211> 142

<212> PRT

<213> Homo sapiens

<400> 37

Leu	Gly	Ser	Met	Cys	Leu	Pro	Val	Glu	Leu	Ser	Gly	Gly	Arg	Cys	Thr
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His	Ser	Ala	Pro	Ser	Gly	Gly	His	Thr	Cys	Cys	Thr	Gly	Gly	Leu	Leu
			20					25					30		
Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro	Val
		35					40					45			
Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu	Asn	Ile
	50					55					60				
Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser
65					70				75					80	
Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr
				85					90					95	
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu
			100					105					110		
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu
	115						120					125			
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu		
	130					135					140				

<210> 38

<211> 173

<212> PRT

<213> Homo sapiens

<400> 38

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val
1				5					10					15	
Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
			20					25					30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
		35					40					45			
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
	50					55					60				
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65					70				75					80	
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
				85					90					95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
			100					105					110		

Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Glu Val
 130 135 140
 Cys Cys Ser Leu Arg Leu Ile Lys Gln Gln Arg Arg Asn Leu Ser Ser
 145 150 155 160
 Pro Cys His Pro Ala Arg Arg Pro Val Leu Ser Pro Lys
 165 170

<210> 39
 <211> 519
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate polynucleotide sequence

<221> misc_feature
 <222> (1)...(519)
 <223> n = A,T,C or G

<400> 39
 atggaytgyc argaraayga rtaytgggag cartggggnm gntgygtnac ntgycarmgn 60
 tgyggncng gncargaryt nwsnaargay tgyggntayg gngarggngg ngaygcntay 120
 tgyacngent gyccnccnmg nmgtayaar wsnwsntggg gncaycayaa rtgycarwsn 180
 tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay 240
 gcngtntgyg gngaytgyyt nccnmgntty taymgnara cnmgnathgg nggnytnar 300
 gaycargart gyathccntg yacnaarcar acnccnacnw sngargtnca rtgygcntty 360
 carytnwsny tngtngargc ngaygcncn acngtnccnc cncargargc nacnytnngtn 420
 gcnytnarg tntgytgyws nytnmgnytn athaarcarc armgmgnaa yytnwsnwsn 480
 cntgycayc cngcnmgnmg nccngtnytn wsncnaar 519

<210> 40
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide ZC26463

<400> 40
 atgcattaac cctcactaaa gggccttcct ggggctcttc ttctct

<210> 41
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide sequence ZC 26464

<400> 41
 taatacgact cactataggg aggggccct gctgctgttg tggat 46

<210> 42
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide ZC24670

<400> 42
 atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca 49

<210> 43
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide sequence ZC 26471

<400> 43
 taatacgact cactataggg agggcccaa ggtctcagct ccagtat 47

<210> 44
 <211> 657
 <212> DNA
 <213> murine

<400> 44
 ggtggcatct ctcttccaat tggctgatt gttggagtga catcactggg tctgctgatg 60
 ttaggactgg tgaactgcat catcctgggtg cagaggaaaa agaagccctc ctgcctacaa 120
 agagatgcca aggtgcctca tgtgcctgat gagaaatccc aggatgcagt aggccttgag 180

cagcagcacc	tgttgaccac	agcaccacagt	tccagcagca	gctccctaga	gagctcagcc	240
agcgctgggg	accgaagggc	gccccctggg	ggccatcccc	aagcaagagt	catggcgagg	300
gcccgaaggt	ttcaggaggc	ccgtgccagc	tccaggattt	cagattcttc	ccacggaagc	360
cacgggaccc	acgtcaacgt	cacctgcac	gtgaacgtct	gtagcagctc	tgaccacagt	420
tctcagtgt	cttcccaagc	cagcgccaca	gtgggagacc	cagatgccaa	gccctcagcg	480
tccccaaggt	atgagcaggt	ccccttctct	caggaggagt	gtccgtctca	gtccccgtgt	540
gagactacag	agacactgca	gagccatgag	aagcccttgc	cccttggtgt	gccggatatg	600
ggcatgaagc	ccagccaagc	tggctgggtt	gatcagattg	cagtcaaagt	ggcctga	657

<210> 45

<211> 824

<212> DNA

<213> Artificial Sequence

<220>

<223> artificial cDNA sequence

<400> 45

ggtaccgaat	tgtacgcgta	tggggacttc	ccatatcaat	cagggacttt	ccgctgggga	60
ctttccggtc	tgactcatgc	ttctgactca	tgcttgggtg	acatcatctc	gactagtcgt	120
accttcccgt	aaatccctcc	ccttcccgga	attacacacg	cgtatttccc	agaaaaggaa	180
ctgtagattt	ctaggaattc	aatccttggc	cacgcgttta	caccggaagt	tttccatatt	240
aggaattcct	tccggtttcc	tttctcgagg	ccaccgtggt	tgagcccagc	actcattcat	300
aaaacgcttg	ttataaaagc	agtggctgcg	gcgcttctgt	actccaaccg	catctgcagc	360
gagcaactga	gaagccaagg	atccaggctg	aattcatggg	tctcaacccc	cagctagtgt	420
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